

5800-79B SEQLIST.TXT

SEQUENCE LISTING

<110> Glucksman, Maria Alexandra
 williamson, Mark
 Tsia, Fong-Ying
 Rudolph-Owen, Laura A.

<120> 22438, 23553, 25278, and 26212 Novel
 Human Sulfatases (A CIP Application)

<130> 35800/208398(5800-79

<150> US 09/495,823

<151> 2000-01-31

<160> 14

<170> FastSEQ for Windows Version 4.0

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<211> 525

<212> PRT

<213> homo sapiens

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Asp Lys Met Ala Ser Glu Gly Met Arg Phe Val Asp Phe His Ala Ala
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 85      90      95
Gly Leu Arg Asn Gly Val Thr Arg Asn Phe Ala Val Thr Ser Val Gly
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Gly Leu Pro Leu Asn Glu Thr Thr Leu Ala Glu Val Leu Gln Ala
115      120      125
Gly Tyr Val Thr Gly Ile Ile Gly Lys Trp His Leu Gly His His Gly
130      135      140
Ser Tyr His Pro Asn Phe Arg Gly Phe Asp Tyr Tyr Phe Gly Ile Pro
145      150      155      160
Tyr Ser His Asp Met Gly Cys Thr Asp Thr Pro Gly Tyr Asn His Pro
165      170      175
Pro Cys Pro Ala Cys Pro Gln Gly Asp Gly Pro Ser Arg Asn Leu Gln
180      185      190
Arg Asp Cys Tyr Thr Asp Val Ala Leu Pro Leu Tyr Glu Asn Leu Asn
195      200      205
Ile Val Glu Gln Pro Val Asn Leu Ser Ser Leu Ala Gln Lys Tyr Ala
210      215      220
Glu Lys Ala Thr Gln Phe Ile Gln Arg Ala Ser Thr Ser Gly Arg Pro
225      230      235      240
Phe Leu Leu Tyr Val Ala Leu Ala His Met His Val Pro Leu Pro Val
245      250      255
Thr Gln Leu Pro Ala Ala Pro Arg Gly Arg Ser Leu Tyr Gly Ala Gly
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Leu Trp Glu Met Asp Ser Leu Val Gly Gln Ile Lys Asp Lys Val Asp
275      280      285

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His Thr Val Lys Glu Asn Thr Phe Leu Trp Phe Thr Gly Asp Asn Gly
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 Pro Trp Ala Gln Lys Cys Glu Leu Ala Gly Ser Val Gly Pro Phe Thr
 305 310 315 320
 Gly Phe Trp Gln Thr Arg Gln Gly Gly Ser Pro Ala Lys Gln Thr Thr
 325 330 335
 Trp Glu Gly Gly His Arg Val Pro Ala Leu Ala Tyr Trp Pro Gly Arg
 340 345 350
 Val Pro Val Asn Val Thr Ser Thr Ala Leu Leu Ser Val Leu Asp Ile
 355 360 365
 Phe Pro Thr Val Val Ala Leu Ala Gln Ala Ser Leu Pro Gln Gly Arg
 370 375 380
 Arg Phe Asp Gly Val Asp Val Ser Glu Val Leu Phe Gly Arg Ser Gln
 385 390 395 400
 Pro Gly His Arg Val Leu Phe His Pro Asn Ser Gly Ala Ala Gly Glu
 405 410 415
 Phe Gly Ala Leu Gln Thr Val Arg Leu Glu Arg Tyr Lys Ala Phe Tyr
 420 425 430
 Ile Thr Gly Gly Ala Arg Ala Cys Asp Gly Ser Thr Gly Pro Glu Leu
 435 440 445
 Gln His Lys Phe Pro Leu Ile Phe Asn Leu Glu Asp Asp Thr Ala Glu
 450 455 460
 Ala Val Pro Leu Glu Arg Gly Gly Ala Glu Tyr Gln Ala Val Leu Pro
 465 470 475 480
 Glu Val Arg Lys Val Leu Ala Asp Val Leu Gln Asp Ile Ala Asn Asp
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 Met Gly Trp Leu Phe Leu Lys Val Leu Leu Ala Gly Val Ser
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 Phe Ser Gly Phe Leu Tyr Pro Leu Val Asp Phe Cys Ile Ser Gly Lys
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 Thr Arg Gly Gln Lys Pro Asn Phe Val Ile Ile Leu Ala Asp Asp Met
 35 40 45

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 Page 2

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cgg Arg 95	ctt Leu	ggc Gly	ctt Leu	cgc Arg	aat Asn 100	gga Gly	gtc Val	aca Thr	cgc Arg	aac Asn 105	ttt Phe	gca Ala	gtc Val	act Thr	tct Ser 110	577
gtg Val	gga Gly	ggc Gly	ctt Leu	ccg Pro 115	ctc Leu	aac Asn	gag Glu	acc Thr	acc Thr 120	ttg Leu	gca Ala	gag Glu	gtg Val	ctg Leu 125	cag Gln	625
cag Gln	gcg Ala	ggt Gly	tac Tyr 130	gtc Val	act Thr	ggg Gly	ata Ile	ata Ile 135	ggc Gly	aaa Lys	tgg Trp	cat His	ctt Leu 140	gga Gly	cac His	673
cac His	ggc Gly	tct Ser 145	tat Tyr	cac His	ccc Pro	aac Asn	ttc Phe 150	cgt Arg	ggt Gly	ttt Phe	gat Asp	tac Tyr 155	tac Tyr	ttt Phe	gga Gly	721
atc Ile	cca Pro 160	tat Tyr	agc Ser	cat His	gat Asp	atg Met 165	ggc Gly	tgt Cys	act Thr	gat Asp	act Thr 170	cca Pro	ggc Gly	tac Tyr	aac Asn	769
cac His 175	cct Pro	cct Pro	tgt Cys	cca Pro	gcg Ala 180	tgt Cys	cca Pro	cag Gln	ggt Gly	gat Asp 185	gga Gly	cca Pro	tca Ser	agg Arg	aac Asn 190	817
ctt Leu	caa Gln	aga Arg	gac Asp	tgt Cys 195	tac Tyr	act Thr	gac Asp	gtg Val	gcc Ala 200	ctc Leu	cct Pro	ctt Leu	tat Tyr	gaa Glu 205	aac Asn	865
ctc Leu	aac Asn	att Ile	gtg Val 210	gag Glu	cag Gln	ccg Pro	gtg Val	aac Asn 215	ttg Leu	agc Ser	agc Ser	ctt Leu	gcc Ala 220	cag Gln	aag Lys	913
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agg Arg	ccc Pro 240	ttc Phe	ctg Leu	ctc Leu	tat Tyr	gtg Val 245	gct Ala	ctg Leu	gcc Ala	cac His	atg Met 250	cac His	gtg Val	ccc Pro	tta Leu	1009
ccc Pro 255	gtg Val	act Thr	cag Gln	cta Leu	cca Pro 260	gca Ala	gcg Ala	cca Pro	cgg Arg	ggc Gly 265	aga Arg	agc Ser	ctg Leu	tat Tyr	ggt Gly 270	1057
gca Ala	ggg Gly	ctc Leu	tgg Trp	gag Glu 275	atg Met	gac Asp	agt Ser	ctg Leu	gtg Val 280	ggc Gly	cag Gln	atc Ile	aag Lys	gac Asp 285	aaa Lys	1105
gtt Val	gac Asp	cac His	aca Thr 290	gtg Val	aag Lys	gaa Glu	aac Asn	aca Thr 295	ttc Phe	ctc Leu	tgg Trp	ttt Phe	aca Thr 300	gga Gly	gac Asp	1153
aat Asn	ggc Gly	ccg Pro 305	tgg Trp	gct Ala	cag Gln	aag Lys	tgt Cys 310	gag Glu	cta Leu	gcg Ala	ggc Gly	agt Ser 315	gtg Val	ggt Gly	ccc Pro	1201

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 65      70      75      80
Phe Val Thr Thr Pro Met Cys Cys Pro Ser Arg Ser Ser Met Leu Thr
 85      90      95
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Asn Glu Tyr Asn Gly Ser Tyr Ile Pro Pro Gly Trp Arg Glu Trp Leu
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Gly Leu Ile Lys Asn Ser Arg Phe Tyr Asn Tyr Thr Val Cys Arg Asn
165      170      175
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Asp Leu Ile Thr Asn Glu Ser Ile Asn Tyr Phe Lys Met Ser Lys Arg
195      200      205
Met Tyr Pro His Arg Pro Val Met Met Val Ile Ser His Ala Ala Pro
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225      230      235      240
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245      250      255
Lys His Trp Ile Met Gln Tyr Thr Gly Pro Met Leu Pro Ile His Met
260      265      270
Glu Phe Thr Asn Ile Leu Gln Arg Lys Arg Leu Gln Thr Leu Met Ser
275      280      285
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Glu Leu Glu Asn Thr Tyr Ile Ile Tyr Thr Ala Asp His Gly Tyr His
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Asp Ile Arg Val Pro Phe Phe Ile Arg Gly Pro Ser Val Glu Pro Gly
340      345      350
Ser Ile Val Pro Gln Ile Val Leu Asn Ile Asp Leu Ala Pro Thr Ile
355      360      365
Leu Asp Ile Ala Gly Leu Asp Thr Pro Pro Asp Val Asp Gly Lys Ser
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Val Leu Lys Leu Leu Asp Pro Glu Lys Pro Gly Asn Arg Phe Arg Thr
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SEQUENCE 1: 1-1000														
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Glu	Glu	Glu	Glu	Leu	Gln	Val	Leu	Gln	Pro	Arg	Asn	Ile	Ala	Lys
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His	Asp	Glu	Gly	His	Lys	Gly	Pro	Arg	Asp	Leu	Gln	Ala	Ser	Ser
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Gly	Asn	Arg	Gly	Arg	Met	Leu	Ala	Asp	Ser	Ser	Asn	Ala	Val	Gly
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665														
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785														
Val	Glu	Arg	Gly	Ile	Leu	Asn	Gln	Leu	His	Val	Gln	Leu	Met	Glu
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                               1 5

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Val Arg Ser Pro Arg Phe Arg Gly Arg Ile Gln Gln Glu Arg Lys Asn
    25                30                35                40

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                45                50                55

ctg ggg tcc ctg caa gtc atg aac aaa acg aga aag att atg gaa cat 725
Leu Gly Ser Leu Gln Val Met Asn Lys Thr Arg Lys Ile Met Glu His
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Gly Gly Ala Thr Phe Ile Asn Ala Phe Val Thr Thr Pro Met Cys Cys
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ccg tca cgg tcc tcc atg ctc acc ggg aag tat gtg cac aat cac aat 821
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Val Tyr Thr Asn Asn Glu Asn Cys Ser Ser Pro Ser Trp Gln Ala Met
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His Glu Pro Arg Thr Phe Ala Val Tyr Leu Asn Asn Thr Gly Tyr Arg
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Thr Ala Phe Phe Gly Lys Tyr Leu Asn Glu Tyr Asn Gly Ser Tyr Ile
                140                145                150

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    155                160                165

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    170                175                180

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aac Asn	att Ile	gac Asp	ttg Leu	gcc Ala 365	ccc Pro	acg Thr	atc Ile	ctg Leu	gat Asp 370	att Ile	gct Ala	ggg Gly	ctc Leu	gac Asp 375	aca Thr	1637
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gat Asp	aca Thr 410	ttc Phe	cta Leu	gtg Val	gaa Glu	aga Arg 415	ggc Gly	aaa Lys	ttt Phe	cta Leu	cgt Arg 420	aag Lys	aag Lys	gaa Glu	gaa Glu	1781
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gtc Val	aaa Lys	gaa Glu	cta Leu	tgc Cys 445	cag Gln	cag Gln	gcc Ala	agg Arg	tac Tyr 450	cag Gln	aca Thr	gcc Ala	tgt Cys	gaa Glu 455	caa Gln	1877

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Ile	His	Lys	Cys	Lys	Gly	Pro	Ser	Asp	Leu	Leu	Thr	Val	Arg	Gln	Ser	
		475					480					485				
acg	cgg	aac	ctc	tac	gct	cgc	ggc	ttc	cat	gac	aaa	gac	aaa	gag	tgc	2021
Thr	Arg	Asn	Leu	Tyr	Ala	Arg	Gly	Phe	His	Asp	Lys	Asp	Lys	Glu	Cys	
	490					495					500					
agt	tgt	agg	gag	tct	ggt	tac	cgt	gcc	agc	aga	agc	caa	aga	aag	agt	2069
Ser	Cys	Arg	Glu	Ser	Gly	Tyr	Arg	Ala	Ser	Arg	Ser	Gln	Arg	Lys	Ser	
505					510					515					520	
caa	cgg	caa	ttc	ttg	aga	aac	cag	ggg	act	cca	aag	tac	aag	ccc	aga	2117
Gln	Arg	Gln	Phe	Leu	Arg	Asn	Gln	Gly	Thr	Pro	Lys	Tyr	Lys	Pro	Arg	
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Phe	Val	His	Thr	Arg	Gln	Thr	Arg	Ser	Leu	Ser	Val	Glu	Phe	Glu	Gly	
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Gln	Pro	Arg	Asn	Ile	Ala	Lys	Arg	His	Asp	Glu	Gly	His	Lys	Gly	Pro	
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Asp	Ser	Ser	Asn	Ala	Val	Gly	Pro	Pro	Thr	Thr	Val	Arg	Val	Thr	His	
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aag	tgt	ttt	att	ctt	ccc	aat	gac	tct	atc	cat	tgt	gag	aga	gaa	ctg	2405
Lys	Cys	Phe	Ile	Leu	Pro	Asn	Asp	Ser	Ile	His	Cys	Glu	Arg	Glu	Leu	
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Tyr	Gln	Ser	Ala	Arg	Ala	Trp	Lys	Asp	His	Lys	Ala	Tyr	Ile	Asp	Lys	
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gag	att	gaa	gct	ctg	caa	gat	aaa	att	aag	aat	tta	aga	gaa	gtg	aga	2501
Glu	Ile	Glu	Ala	Leu	Gln	Asp	Lys	Ile	Lys	Asn	Leu	Arg	Glu	Val	Arg	
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Gly	His	Leu	Lys	Arg	Arg	Lys	Pro	Glu	Glu	Cys	Ser	Cys	Ser	Lys	Gln	
665				670						675					680	
agc	tat	tac	aat	aaa	gag	aaa	ggt	gta	aaa	aag	caa	gag	aaa	tta	aag	2597
Ser	Tyr	Tyr	Asn	Lys	Glu	Lys	Gly	Val	Lys	Lys	Gln	Glu	Lys	Leu	Lys	
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agc	cat	ctt	cac	cca	ttc	aag	gag	gct	gct	cag	gaa	gta	gat	agc	aaa	2645
Ser	His	Leu	His	Pro	Phe	Lys	Glu	Ala	Ala	Gln	Glu	Val	Asp	Ser	Lys	
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Leu Gln Leu Phe Lys Glu Asn Asn Arg Arg Arg Lys Lys Glu Arg Lys	
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gag aag aga cgg cag agg aag ggg gaa gag tgc agc ctg cct ggc ctc	2741
Glu Lys Arg Arg Gln Arg Lys Gly Glu Glu Cys Ser Leu Pro Gly Leu	
730 735 740	
act tgc ttc acg cat gac aac aac cac tgg cag aca gcc ccg ttc tgg	2789
Thr Cys Phe Thr His Asp Asn Asn His Trp Gln Thr Ala Pro Phe Trp	
745 750 755 760	
aac ctg gga tct ttc tgt gct tgc acg agt tct aac aat aac acc tac	2837
Asn Leu Gly Ser Phe Cys Ala Cys Thr Ser Ser Asn Asn Asn Thr Tyr	
765 770 775	
tgg tgt ttg cgt aca gtt aat gag acg cat aat ttt ctt ttc tgt gag	2885
Trp Cys Leu Arg Thr Val Asn Glu Thr His Asn Phe Leu Phe Cys Glu	
780 785 790	
ttt gct act ggc ttt ttg gag tat ttt gat atg aat aca gat cct tat	2933
Phe Ala Thr Gly Phe Leu Glu Tyr Phe Asp Met Asn Thr Asp Pro Tyr	
795 800 805	
cag ctc aca aat aca gtg cac acg gta gaa cga ggc att ttg aat cag	2981
Gln Leu Thr Asn Thr Val His Thr Val Glu Arg Gly Ile Leu Asn Gln	
810 815 820	
cta cac gta caa cta atg gag ctc aga agc tgt caa gga tat aag cag	3029
Leu His Val Gln Leu Met Glu Leu Arg Ser Cys Gln Gly Tyr Lys Gln	
825 830 835 840	
tgc aac cca aga cct aag aat ctt gat gtt gga aat aaa gat gga gga	3077
Cys Asn Pro Arg Pro Lys Asn Leu Asp Val Gly Asn Lys Asp Gly Gly	
845 850 855	
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Ser Tyr Asp Leu His Arg Gly Gln Leu Trp Asp Gly Trp Glu Gly *	
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Gly	Glu	Ala	Gly	Glu	Gln	Pro	Ser	Ala	Ala	Pro	Pro	Gln	Pro	Pro	His
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Gly	Val	Lys	Leu	Glu	Asn	Tyr	Tyr	Ile	Gln	Pro	Ile	Cys	Thr	Pro	Ser
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His	Ser	Ile	Ile	Arg	Pro	Gln	Gln	Pro	Asn	Cys	Leu	Pro	Leu	Asp	Gln
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Arg	Arg	Gly	Phe	Asp	Thr	Phe	Leu	Gly	Ser	Leu	Thr	Gly	Asn	Val	Asp
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Leu	His	Glu	Gly	Glu	Asn	Val	Ala	Trp	Gly	Leu	Ser	Gly	Gln	Tyr	Ser
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Thr	Met	Leu	Tyr	Ala	Gln	Arg	Ala	Ser	His	Ile	Leu	Ala	Ser	His	Ser
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Pro	Leu	Gln	Ser	Pro	Arg	Glu	Tyr	Leu	Tyr	Arg	Tyr	Arg	Thr	Met	Gly
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Asn	Val	Ala	Arg	Arg	Lys	Tyr	Ala	Ala	Met	Val	Thr	Cys	Met	Asp	Glu
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Thr	Leu	Val	Gly	Leu	Ala	Gly	Gly	Thr	Thr	Ser	Ala	Ala	Asp	Gly	Leu
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Asp	Gly	Tyr	Asp	Val	Trp	Pro	Ala	Ile	Ser	Glu	Gly	Arg	Ala	Ser	Pro
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Arg	Thr	Glu	Ile	Leu	His	Asn	Ile	Asp	Pro	Leu	Tyr	Asn	His	Ala	Gln
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His	Gly	Ser	Leu	Glu	Gly	Gly	Phe	Gly	Ile	Trp	Asn	Thr	Ala	Val	Gln
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Ala	Ala	Ile	Arg	Val	Gly	Glu	Trp	Lys	Leu	Leu	Thr	Gly	Asp	Pro	Gly
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Tyr	Gly	Asp	Trp	Ile	Pro	Pro	Gln	Thr	Leu	Ala	Thr	Phe	Pro	Gly	Ser
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Trp	Trp	Asn	Leu	Glu	Arg	Met	Ala	Ser	Val	Arg	Gln	Ala	Val	Trp	Leu
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Phe	Asn	Ile	Ser	Ala	Asp	Pro	Tyr	Glu	Arg	Glu	Asp	Leu	Ala	Gly	Gln
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Arg	Thr	Ala	Ile	Pro	Val	Arg	Tyr	Pro	Ala	Glu	Asn	Pro	Arg	Ala	His
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Pro	Asp	Phe	Asn	Gly	Gly	Ala	Trp	Gly	Pro	Trp	Ala	Ser	Asp	Glu	Glu
		515					520					525			
Glu	Glu	Glu	Glu	Glu	Gly	Arg	Ala	Arg	Ser	Phe	Ser	Arg	Gly	Arg	Arg
	530					535					540				
Lys	Lys	Lys	Cys	Lys	Ile	Cys	Lys	Leu	Arg	Ser	Phe	Phe	Arg	Lys	Leu
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gcgggcctga	cctccccaga	gcgccccgct	gcggccgagc	agatccggcc	cagccgtccg	180
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Ser Leu Val	Ser Leu Leu	Ser Phe	Gly Tyr	Leu Ser	Trp Asp	Trp Ala
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Lys Pro Ser	Phe Val Ala	Asp Gly	Pro Gly	Glu Ala	Gly Glu	Gln Pro
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tcg gcc gct	ccg ccc cag	cct ccc	cac atc	atc atc	ttc atc	ctc acg
Ser Ala Ala	Pro Pro Gln	Pro Pro	His Ile	Ile Ile	Phe Ile	Leu Thr
	40		45		50	
gac caa ggc	tac cac gac	gtg ggc	tac cat	ggt tca	gat atc	gag acc
Asp Gln Gly	Tyr His Asp	Val Gly	Tyr His	Gly Ser	Asp Ile	Glu Thr
	60		65		70	
cct acg ctg	gac agg ctg	gcg gcc	aag ggg	gtc aag	ttg gag	aat tat
Pro Thr Leu	Asp Arg Leu	Ala Ala	Lys Gly	Val Lys	Leu Glu	Asn Tyr
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tac atc cag	ccc atc tgc	acg cct	tcg cgg	agc cag	ctc ctc	act ggc
Tyr Ile Gln	Pro Ile Cys	Thr Pro	Ser Arg	Ser Gln	Leu Leu	Thr Gly
	90		95		100	
agg tac cag	atc cac aca	gga ctc	cag cat	tcc atc	atc cgc	cca cag
Arg Tyr Gln	Ile His Thr	Gly Leu	Gln His	Ser Ile	Ile Arg	Pro Gln
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cag Gln	gag Glu	gca Ala	ggt Gly	tat Tyr 140	tcc Ser	acc Thr	cat His	atg Met	gtg Val 145	ggc Gly	aag Lys	tgg Trp	cac His	ctg Leu 150	ggc Gly	786
ttc Phe	tac Tyr	cgg Arg	aag Lys 155	gag Glu	tgt Cys	ctg Leu	ccc Pro	acc Thr 160	cgt Arg	cgg Arg	ggc Gly	ttc Phe	gac Asp 165	acc Thr	ttc Phe	834
ctg Leu	ggc Gly	tgc Ser 170	ctc Leu	acg Thr	ggc Gly	aat Asn	gtg Val 175	gac Asp	tat Tyr	tac Tyr	acc Thr	tat Tyr 180	gac Asp	aac Asn	tgt Cys	882
gat Asp	ggc Gly 185	cca Pro	ggc Gly	gtg Val	tgc Cys 190	ggc Gly	ttc Phe	gac Asp	ctg Leu	cac His	gag Glu 195	ggt Gly	gag Glu	aat Asn	gtg Val	930
gcc Ala 200	tgg Trp	ggg Gly	ctc Leu	agc Ser	ggc Gly 205	cag Gln	tac Tyr	tcc Ser	act Thr	atg Met 210	ctt Leu	tac Tyr	gcc Ala	cag Gln	cgc Arg 215	978
gcc Ala	agc Ser	cat His	atc Ile	ctg Leu 220	gcc Ala	agc Ser	cac His	agc Ser	cct Pro 225	cag Gln	cgt Arg	ccc Pro	ctc Leu	ttc Phe 230	ctc Leu	1026
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gcc Ala 280	ctc Leu	aag Lys	cgc Arg	tac Tyr	ggt Gly 285	ttc Phe	tac Tyr	aac Asn	aac Asn	agt Ser 290	gtc Val	atc Ile	atc Ile	ttc Phe	tcc Ser 295	1218
agt Ser	gac Asp	aat Asn	ggt Gly	ggc Gly 300	cag Gln	act Thr	ttc Phe	tgc Ser	ggg Gly 305	ggc Gly	agc Ser	aac Asn	tgg Trp	ccg Pro 310	ctc Leu	1266
cga Arg	gga Gly	cgc Arg	aag Lys 315	ggc Gly	act Thr	tat Tyr	tgg Trp	gaa Glu 320	ggt Gly	ggc Gly	gtg Val	cgg Arg	ggc Gly 325	cta Leu	ggc Gly	1314
ttt Phe	gtc Val	cac His 330	agt Ser	ccc Pro	ctg Leu	ctc Leu	aag Lys 335	cga Arg	aag Lys	caa Gln	cgg Arg	aca Thr 340	agc Ser	cgg Arg	gca Ala	1362
ctg Leu	atg Met 345	cac His	atc Ile	act Thr	gac Asp	tgg Trp 350	tac Tyr	ccg Pro	acc Thr	ctg Leu	gtg Val 355	ggt Gly	ctg Leu	gca Ala	ggt Gly	1410
ggt Gly 360	acc Thr	acc Thr	tca Ser	gca Ala	gcc Ala 365	gat Asp	ggg Gly	cta Leu	gat Asp	ggc Gly 370	tac Tyr	gac Asp	gtg Val	tgg Trp	ccg Pro 375	1458

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Ile Asp Pro Leu Tyr Asn His Ala Gln His Gly Ser Leu Glu Gly Gly	
395 400 405	
ttt ggc atc tgg aac acc gcc gtg cag gct gcc atc cgc gtg ggt gag	1602
Phe Gly Ile Trp Asn Thr Ala Val Gln Ala Ile Arg Val Gly Glu	
410 415 420	
tgg aag ctg ctg aca gga gac ccc ggc tat ggc gat tgg atc cca ccg	1650
Trp Lys Leu Leu Thr Gly Asp Pro Gly Tyr Gly Asp Trp Ile Pro Pro	
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cag aca ctg gcc acc ttc ccg ggt agc tgg tgg aac ctg gaa cga atg	1698
Gln Thr Leu Ala Thr Phe Pro Gly Ser Trp Trp Asn Leu Glu Arg Met	
440 445 450 455	
gcc agt gtc cgc cag gcc gtg tgg ctc ttc aac atc agt gct gac cct	1746
Ala Ser Val Arg Gln Ala Val Trp Leu Phe Asn Ile Ser Ala Asp Pro	
460 465 470	
tat gaa cgg gag gac ctg gct ggc cag cgg cct gat gtg gtc cgc acc	1794
Tyr Glu Arg Glu Asp Leu Ala Gly Gln Arg Pro Asp Val Val Arg Thr	
475 480 485	
ctg ctg gct cgc ctg gcc gaa tat aac cgc aca gcc atc ccg gta cgc	1842
Leu Leu Ala Arg Leu Ala Glu Tyr Asn Arg Thr Ala Ile Pro Val Arg	
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Tyr Pro Ala Glu Asn Pro Arg Ala His Pro Asp Phe Asn Gly Gly Ala	
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Trp Gly Pro Trp Ala Ser Asp Glu Glu Glu Glu Glu Glu Glu Gly Arg	
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Ala Arg Ser Phe Ser Arg Gly Arg Arg Lys Lys Lys Cys Lys Ile Cys	
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Lys Leu Arg Ser Phe Phe Arg Lys Leu Asn Thr Arg Leu Met Ser Gln	
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gaccttcttg ggtcttcaca tggcctaggc cagtcctccg gtcagactgg tgtcaggcac	2623
cgtggtgcaa aattcctctt ctggccctc cagtaccag agaaaactggc tgggccatta	2683

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acctgcaagt	ggggatgcca	gccctggctc	tgccctcttc	atgaggctct	ggaagactgg	2863
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Phe	Trp	Ile	Leu	Cys	Leu	Leu	Thr	Tyr	Gly	Tyr	Leu	Ser	Trp	Gly	Gln
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Ala	Leu	Glu	Glu	Glu	Glu	Gly	Ala	Leu	Leu	Ala	Gln	Ala	Gly	Glu	
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Lys	Leu	Glu	Pro	Ser	Thr	Thr	Ser	Thr	Ser	Gln	Pro	His	Leu	Ile	Phe
65					70				75					80	
Ile	Leu	Ala	Asp	Asp	Gln	Gly	Phe	Arg	Asp	Val	Gly	Tyr	His	Gly	Ser
			85					90					95		
Glu	Ile	Lys	Thr	Pro	Thr	Leu	Asp	Lys	Leu	Ala	Ala	Glu	Gly	Val	Lys
			100					105					110		
Leu	Glu	Asn	Tyr	Tyr	Val	Gln	Pro	Ile	Cys	Thr	Pro	Ser	Arg	Ser	Gln
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Phe	Ile	Thr	Gly	Lys	Tyr	Gln	Ile	His	Thr	Gly	Leu	Gln	His	Ser	Ile
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Ile	Arg	Pro	Thr	Gln	Pro	Asn	Cys	Leu	Pro	Leu	Asp	Asn	Ala	Thr	Leu
145					150					155					160
Pro	Gln	Lys	Leu	Lys	Glu	Val	Gly	Tyr	Ser	Thr	His	Met	Val	Gly	Lys
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Trp	His	Leu	Gly	Phe	Tyr	Arg	Lys	Glu	Cys	Met	Pro	Thr	Arg	Arg	Gly
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Phe	Asp	Thr	Phe	Phe	Gly	Ser	Leu	Leu	Gly	Ser	Gly	Asp	Tyr	Tyr	Thr
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His	Tyr	Lys	Cys	Asp	Ser	Pro	Gly	Met	Cys	Gly	Tyr	Asp	Leu	Tyr	Glu
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Asn	Asp	Asn	Ala	Ala	Trp	Asp	Tyr	Asp	Asn	Gly	Ile	Tyr	Ser	Thr	Gln
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Lys	Pro	Ile	Phe	Leu	Tyr	Ile	Ala	Tyr	Gln	Ala	Val	His	Ser	Pro	Leu
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Gln	Ala	Pro	Gly	Arg	Tyr	Phe	Glu	His	Tyr	Arg	Ser	Ile	Ile	Asn	Ile
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Asn	Arg	Arg	Arg	Tyr	Ala	Ala	Met	Leu	Ser	Cys	Leu	Asp	Glu	Ala	Ile
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Asn	Asn	Val	Thr	Leu	Ala	Leu	Lys	Thr	Tyr	Gly	Phe	Tyr	Asn	Asn	Ser
305					310					315					320
Ile	Ile	Ile	Tyr	Ser	Ser	Asp	Asn	Gly	Gly	Gln	Pro	Thr	Ala	Gly	Gly
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Ser	Asn	Trp	Pro	Leu	Arg	Gly	Ser	Lys	Gly	Thr	Tyr	Trp	Glu	Gly	Gly
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Thr	Val	Cys	Lys	Glu	Leu	Val	His	Ile	Thr	Asp	Trp	Tyr	Pro	Thr	Leu
	370					375					380				
Ile	Ser	Leu	Ala	Glu	Gly	Gln	Ile	Asp	Glu	Asp	Ile	Gln	Leu	Asp	Gly
385					390					395					400
Tyr	Asp	Ile	Trp	Glu	Thr	Ile	Ser	Glu	Gly	Leu	Arg	Ser	Pro	Arg	Val

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 Asp Ile Leu His Asn Ile Asp Pro Ile Tyr Thr Lys Ala Lys Asn Gly
 420 425 430
 Ser Trp Ala Ala Gly Tyr Gly Ile Trp Asn Thr Ala Ile Gln Ser Ala
 435 440 445
 Ile Arg Val Gln His Trp Lys Leu Leu Thr Gly Asn Pro Gly Tyr Ser
 450 455 460
 Asp Trp Val Pro Pro Gln Ser Phe Ser Asn Leu Gly Pro Asn Arg Trp
 465 470 475 480
 His Asn Glu Arg Ile Thr Leu Ser Thr Gly Lys Ser Val Trp Leu Phe
 485 490 495
 Asn Ile Thr Ala Asp Pro Tyr Glu Arg Val Asp Leu Ser Asn Arg Tyr
 500 505 510
 Pro Gly Ile Val Lys Lys Leu Leu Arg Arg Leu Ser Gln Phe Asn Lys
 515 520 525
 Thr Ala Val Pro Val Arg Tyr Pro Pro Lys Asp Pro Arg Ser Asn Pro
 530 535 540
 Arg Leu Asn Gly Gly Val Trp Gly Pro Trp Tyr Lys Glu Glu Thr Lys
 545 550 555 560
 Lys Lys Lys Pro Ser Lys Asn Gln Ala Glu Lys Lys Gln Lys Lys Ser
 565 570 575
 Lys Lys Lys Lys Lys Lys Gln Gln Lys Ala Val Ser Gly Ser Thr Cys
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 His Ser Gly Val Thr Cys Gly
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 agccctcctt gttcttccgg agtcccattc attagccat cacttctgga agattaaagt 180
 tgtcggacat ggtgacagct gagaggagag gaggatttct tgccagggtg agagtcttca 240
 ccgtctgttg ggtgcatgtg tgcgcccgca gcggcgcggg gcgctgtggt ctccgcgtgg 300
 agtctcacct gggacctgag tga atg gct ccc agg ggc tgt gcg ggg cat ccg 353
 Met Ala Pro Arg Gly Cys Ala Gly His Pro
 1 5 10
 cct ccg cct tct cca cag gcc tgt gtc tgt cct gga aag atg cta gca 401
 Pro Pro Pro Ser Pro Gln Ala Cys Val Cys Pro Gly Lys Met Leu Ala
 15 20 25
 atg ggg gcg ctg gca gga ttc tgg atc ctc tgc ctc ctc act tat ggt 449
 Met Gly Ala Leu Ala Gly Phe Trp Ile Leu Cys Leu Leu Thr Tyr Gly
 30 35 40
 tac ctg tcc tgg ggc cag gcc tta gaa gag gag gaa gaa ggg gcc tta 497
 Tyr Leu Ser Trp Gly Gln Ala Leu Glu Glu Glu Glu Gly Ala Leu
 45 50 55
 cta gct caa gct gga gag aaa cta gag ccc agc aca act tcc acc tcc 545
 Leu Ala Gln Ala Gly Glu Lys Leu Glu Pro Ser Thr Thr Ser Thr Ser
 60 65 70
 cag ccc cat ctc att ttc atc cta gcg gat gat cag gga ttt aga gat 593
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gct Ala	gcc Ala	gaa Glu	gga Gly 110	gtt Val	aaa Lys	ctg Leu	gag Glu	aac Asn 115	tac Tyr	tat Tyr	gtc Val	cag Gln	cct Pro 120	att Ile	tgc Cys	689
aca Thr	cca Pro	tcc Ser 125	agg Arg	agt Ser	cag Gln	ttt Phe	att Ile 130	act Thr	gga Gly	aag Lys	tat Tyr	cag Gln 135	ata Ile	cac His	acc Thr	737
gga Gly	ctt Leu 140	caa Gln	cat His	tct Ser	atc Ile	ata Ile 145	aga Arg	cct Pro	acc Thr	caa Gln	ccc Pro 150	aac Asn	tgt Cys	tta Leu	cct Pro	785
ctg Leu 155	gac Asp	aat Asn	gcc Ala	acc Thr	cta Leu 160	cct Pro	cag Gln	aaa Lys	ctg Leu	aag Lys 165	gag Glu	gtt Val	gga Gly	tat Tyr	tca Ser 170	833
acg Thr	cat His	atg Met	gtc Val	gga Gly 175	aaa Lys	tgg Trp	cac His	ttg Leu	ggt Gly 180	ttt Phe	tac Tyr	aga Arg	aaa Lys	gaa Glu 185	tgc Cys	881
atg Met	ccc Pro	acc Thr	aga Arg 190	aga Arg	gga Gly	ttt Phe	gat Asp	acc Thr 195	ttt Phe	ttt Phe	ggt Gly	tcc Ser	ctt Leu 200	ttg Leu	gga Gly	929
agt Ser	ggg Gly	gat Asp 205	tac Tyr	tat Tyr	aca Thr	cac His	tac Tyr 210	aaa Lys	tgt Cys	gac Asp	agt Ser	cct Pro 215	ggg Gly	atg Met	tgt Cys	977
ggc Gly	tat Tyr 220	gac Asp	ttg Leu	tat Tyr	gaa Glu	aac Asn 225	gac Asp	aat Asn	gct Ala	gcc Ala	tgg Trp 230	gac Asp	tat Tyr	gac Asp	aat Asn	1025
ggc Gly 235	ata Ile	tac Tyr	tcc Ser	aca Thr	cag Gln 240	atg Met	tac Tyr	act Thr	cag Gln	aga Arg 245	gta Val	cag Gln	caa Gln	atc Ile	tta Leu 250	1073
gct Ala	tcc Ser	cat His	aac Asn	ccc Pro 255	aca Thr	aag Lys	cct Pro	ata Ile	ttt Phe 260	tta Leu	tat Tyr	att Ile	gcc Ala	tat Tyr 265	caa Gln	1121
gct Ala	gtt Val	cat His	tca Ser 270	cca Pro	ctg Leu	caa Gln	gct Ala	cct Pro 275	ggc Gly	agg Arg	tat Tyr	ttc Phe	gaa Glu 280	cac His	tac Tyr	1169
cga Arg	tcc Ser	att Ile 285	atc Ile	aac Asn	ata Ile	aac Asn	agg Arg 290	agg Arg	aga Arg	tat Tyr	gct Ala	gcc Ala 295	atg Met	ctt Leu	tcc Ser	1217
tgc Cys	tta Leu 300	gat Asp	gaa Glu	gca Ala	atc Ile	aac Asn 305	aac Asn	gtg Val	aca Thr	ttg Leu	gct Ala 310	cta Leu	aag Lys	act Thr	tat Tyr	1265
ggt Gly 315	ttc Phe	tat Tyr	aac Asn	aac Asn	agc Ser 320	att Ile	atc Ile	att Ile	tac Tyr	tct Ser 325	tca Ser	gat Asp	aat Asn	ggt Gly	ggc Gly 330	1313

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Thr	Tyr	Trp	Glu	Gly	Gly	Ile	Arg	Ala	Val	Gly	Phe	Val	His	Ser	Pro	
			350					355					360			
ctt	ctg	aaa	aac	aag	gga	aca	gtg	tgt	aag	gaa	ctt	gtg	cac	atc	act	1457
Leu	Leu	Lys	Asn	Lys	Gly	Thr	Val	Cys	Lys	Glu	Leu	Val	His	Ile	Thr	
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Asp	Trp	Tyr	Pro	Thr	Leu	Ile	Ser	Leu	Ala	Glu	Gly	Gln	Ile	Asp	Glu	
	380					385					390					
gac	att	caa	cta	gat	ggc	tat	gat	atc	tgg	gag	acc	ata	agt	gag	ggt	1553
Asp	Ile	Gln	Leu	Asp	Gly	Tyr	Asp	Ile	Trp	Glu	Thr	Ile	Ser	Glu	Gly	
	395				400					405					410	
ctt	cgc	tca	ccc	cga	gta	gat	att	ttg	cat	aac	att	gac	ccc	ata	tac	1601
Leu	Arg	Ser	Pro	Arg	Val	Asp	Ile	Leu	His	Asn	Ile	Asp	Pro	Ile	Tyr	
				415					420					425		
acc	aag	gca	aaa	aat	ggc	tcc	tgg	gca	gca	ggc	tat	ggg	atc	tgg	aac	1649
Thr	Lys	Ala	Lys	Asn	Gly	Ser	Trp	Ala	Ala	Gly	Tyr	Gly	Ile	Trp	Asn	
			430					435					440			
act	gca	atc	cag	tca	gcc	atc	aga	gtg	cag	cac	tgg	aaa	ttg	ctt	aca	1697
Thr	Ala	Ile	Gln	Ser	Ala	Ile	Arg	Val	Gln	His	Trp	Lys	Leu	Leu	Thr	
		445					450					455				
gga	aat	cct	ggc	tac	agc	gac	tgg	gtc	ccc	cct	cag	tct	ttc	agc	aac	1745
Gly	Asn	Pro	Gly	Tyr	Ser	Asp	Trp	Val	Pro	Pro	Gln	Ser	Phe	Ser	Asn	
	460					465					470					
ctg	gga	ccg	aac	cgg	tgg	cac	aat	gaa	cgg	atc	acc	ttg	tca	act	ggc	1793
Leu	Gly	Pro	Asn	Arg	Trp	His	Asn	Glu	Arg	Ile	Thr	Leu	Ser	Thr	Gly	
	475				480					485					490	
aaa	agt	gta	tgg	ctt	ttc	aac	atc	aca	gcc	gac	cca	tat	gag	agg	gtg	1841
Lys	Ser	Val	Trp	Leu	Phe	Asn	Ile	Thr	Ala	Asp	Pro	Tyr	Glu	Arg	Val	
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gac	cta	tct	aac	agg	tat	cca	gga	atc	gtg	aag	aag	ctc	cta	cgg	agg	1889
Asp	Leu	Ser	Asn	Arg	Tyr	Pro	Gly	Ile	Val	Lys	Lys	Leu	Leu	Arg	Arg	
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Leu	Ser	Gln	Phe	Asn	Lys	Thr	Ala	Val	Pro	Val	Arg	Tyr	Pro	Pro	Lys	
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gac	ccc	aga	agt	aac	cct	agg	ctc	aat	gga	ggg	gtc	tgg	gga	cca	tgg	1985
Asp	Pro	Arg	Ser	Asn	Pro	Arg	Leu	Asn	Gly	Gly	Val	Trp	Gly	Pro	Trp	
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Tyr	Lys	Glu	Glu	Thr	Lys	Lys	Lys	Lys	Pro	Ser	Lys	Asn	Gln	Ala	Glu	
	555				560					565					570	
aaa	aag	caa	aag	aaa	agc	aaa	aaa	aag	aag	aag	aaa	cag	cag	aaa	gca	2081
Lys	Lys	Gln	Lys	Lys	Ser	Lys	Lys	Lys	Lys	Lys	Lys	Gln	Gln	Lys	Ala	
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 <212> PRT
 <213> Artificial Sequence

<220>
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 20 25 30
 Ala Glu Glu Gly Leu Arg Phe Thr Asn Ala Tyr Val Thr Pro Leu
 35 40 45
 Cys Thr Pro Ser Arg Ala Ala Leu Leu Thr Gly Arg Tyr Pro His Arg
 50 55 60
 Thr Gly Met Tyr Thr Asn Asn Arg Ala Gly Val Leu Pro Phe Thr Gly
 65 70 75 80
 Trp Ser Leu Glu Gly Gly Leu Pro Leu Asp Glu Thr Thr Leu Pro Glu
 85 90 95
 Leu Leu Lys Glu Ala Gly Tyr Ala Thr Gly Met Val Gly Lys Trp His
 100 105 110
 Gly Tyr Asn Glu Glu Ser Ser Ala Ser Asp Phe Ala His Leu Pro Leu
 115 120 125
 Gly Arg Gly Phe Asp Tyr Phe Tyr Gly Asn Leu Gly Gly Glu Asp Gln
 130 135 140
 Trp Tyr Pro Leu Val Asp Ala Leu Leu Pro Phe Thr Asn Asp Thr Tyr
 145 150 155 160
 Thr Cys Glu Gly Gly Tyr Gly Phe Ser Lys Asp Val Ala Leu Lys Pro
 165 170 175
 Leu Gly Ala Leu Gly Val Asn Glu Val Glu Ala Pro Asp Lys Ala Leu
 180 185 190
 Ala Asp Tyr Lys Thr Ala Gly Ala Leu Asn Val Pro His His Val Phe
 195 200 205
 Glu Trp Ala Asp Arg Tyr Ala Gly Ala Val Asp Val Gly Arg Pro Phe
 210 215 220
 Leu Ala Val Leu Ile Phe Pro Arg Pro Ala Ala Cys Phe Leu Tyr Pro
 225 230 235 240
 Asn Ala Thr Val Val Ser Gln Pro Met Pro His Ser Pro Leu Thr Ala
 245 250 255
 Pro Arg Pro Trp Gln Leu Leu Ala Asp Glu Ala Leu Pro Phe Leu Glu
 260 265 270
 Arg Asn Gly Gln Arg Asp Lys Pro Phe Phe Leu Tyr Leu Ser Tyr Lys
 275 280 285
 His Val His Ile Pro Arg Asp Ala Pro Met Leu Phe Ser Ser Lys Asp
 290 295 300
 Phe Ala Gly Ser Ser Arg Arg Gly Leu Tyr Gly Leu Ile Leu Asp Ser
 305 310 315 320
 Val Glu Glu Met Asp Asp Gly Val Gly Arg Val Leu Asn Ala Leu Asp
 325 330 335
 Glu Leu Asn Gly Leu Leu Asp Asn Thr Leu Ile Ile Phe Thr Ser Leu
 340 345 350
 Leu Asp His Gly Gly His Leu Gly Ala His Gly His Leu Gly Ile Arg

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 Tyr 370 Glu Gly Gly Thr Arg 375 Val Pro Leu Ile Val 380 Arg Trp Pro Glu Gly
 Ile 385 Ile Ala Pro Gly 390 Gln Val Ser Asp Glu 395 Leu Val Ser Leu Met Asp
 Leu Phe Pro Thr 405 Ile Leu Asp Leu Ala 410 Gly Ala Pro Leu Pro Gly Val
 Ala Ala Gly 420 Val Lys Asp Arg Ile 425 Leu Asp Gly Val Ser 430 Leu Leu Pro
 Leu 435 Leu Gly Ala Ala Gly 440 Ser Ser Arg His Glu 445 Thr Leu Phe Tyr
 Glu 450 Ser Tyr Cys Asn Glu 455 Arg Gly Phe Leu 460 Pro Ala Val Arg Trp
 465 Gly Lys Lys Lys Ala His 470 Phe Arg Thr Pro Asn Ile Ala Gly Trp Gln
 Arg Val Asp Phe 485 Asp Asp Val Trp Lys 490 Leu Phe Asn Thr Val Glu Asp
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<223> Pfam consensus sequence for human sulfatase

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 Cys Ser Pro Ser Arg Ala Ala Leu Leu Thr Gly Arg Tyr Pro His Arg
 35 50 His Gly Met Val Ser Asn Gly Arg Leu Gly Val 60 Leu Gly Phe Thr Ala
 65 Lys Ser Gly Gly Leu Pro Leu Asp Glu Thr Thr Leu Pro Glu Leu Leu
 85 Lys Glu Ala Gly Tyr Ala Thr Gly Leu Val Gly Lys Trp His Leu Gly
 100 Leu Asn Glu Asn Ser Asp Ala Ala Gly Asp Gly Glu His 110 Pro Leu
 Gly Trp Arg Gly Phe Asp Tyr Phe Asp Gly Phe Leu Tyr Gly Ser Pro
 115 130 Phe Thr Tyr Asp Glu Glu 135 Asn Cys Asp Asn Gly 140 Glu Gly Thr Glu Pro
 145 Pro Glu Ala Tyr Pro Glu Gln Gly Trp Leu Pro Gln Ile Leu Gly Tyr
 Tyr Leu Thr Asp 165 Leu Leu Ala Asp Lys 170 Ala Leu Gly Leu Leu Asp Val
 Ala Ser Ala Ala Gly Arg Leu Leu Ala Lys Ala Leu Ala Ala Ser Arg
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 200

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Glu	Lys	Pro	Phe	Phe	Leu	Tyr	Leu	Ala	Phe	Leu	Arg	Leu	His	Val	His	
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Thr	Pro	Leu	Phe	Ser	Pro	Ala	Glu	Asp	Leu	Glu	Ser	Lys	Asp	Phe	Leu	
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Gly	Arg	Ser	Gln	Arg	Gly	Arg	Tyr	Gly	Asp	Leu	Val	Glu	Glu	Met	Asp	
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Asp	Leu	Val	Gly	Arg	Val	Leu	Asp	Ala	Leu	Glu	Asp	Leu	Gly	Leu	Leu	
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Asp	Asn	Thr	Leu	Val	Ile	Phe	Thr	Ser	Asp	Asn	Gly	Ala	His	Leu	Glu	
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Gly	Thr	Pro	Glu	Trp	Tyr	Gly	Gly	Gly	Asn	Gly	Pro	Leu	Lys	Gly	Gly	
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Val	Arg	Trp	Pro	Gly	Gly	Ile	Ala	Pro	Ala	Gly	Arg	Val	Lys	Glu	Lys	
370						375					380					
Ser	Glu	Leu	Val	Ser	His	Val	Asp	Leu	Ala	Pro	Thr	Ile	Leu	Asp	Leu	
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Ala	Gly	Ala	Pro	Leu	Pro	Lys	Val	Ala	Asn	Gly	Ala	Lys	Asp	Arg	Pro	
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Leu	Asp	Gly	Val	Ser	Leu	Leu	Pro	Leu	Leu	Leu	Gly	Gly	Ala	Ala	Pro	
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Ser	Arg	Arg	Ala	His	Glu	Thr	Leu	Phe	His	Tyr	Asn	Gly	Lys	Gly	Arg	
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Lys	Leu	Arg	Ala	Val	Arg	Trp	Pro	Arg	Lys	Ser	Gly	Lys	Thr	Pro	Lys	
		450				455					460					
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Gly	Trp	Glu	Cys	Val	Gly	Thr	Val	Ser	Gln	Ala	Asp	Asp	Ile	Glu	Asp	
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Cys	Arg	Cys	Glu	Gly	Val	Glu	Thr	Val	Thr	His	His	Asp	Pro	Glu		
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attttggccg	atgacatggg	gtggggtgac	ctgggagcaa	actgggcaga	aacaaaggac											180
actgccaacc	ttgataagat	ggcttcggag	ggaatgaggt	ttgtggattt	ccatgcagct											240
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